

1600 #17

Serial Number: 09/728,4210

CRF Processing Date: 8/21/2002
 Edited by:
 Verified by: (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____



1600

RAW SEQUENCE LISTING

DATE: 08/20/2002

PATENT APPLICATION: US/09/728,421D

TIME: 12:49:42

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

5 <110> APPLICANT: Yoshinaga, Steven
 9 <120> TITLE OF INVENTION: Novel Polypeptides Involved in Immune Response
 13 <130> FILE REFERENCE: A-579D
 17 <140> CURRENT APPLICATION NUMBER: 09/728,421D
 19 <141> CURRENT FILING DATE: 2000-11-28
 23 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
 25 <151> PRIOR FILING DATE: 2000-01-27
 29 <150> PRIOR APPLICATION NUMBER: US 09/264,527
 31 <151> PRIOR FILING DATE: 1999-03-08
 35 <150> PRIOR APPLICATION NUMBER: US 09/244,448
 37 <151> PRIOR FILING DATE: 1999-02-03
 41 <160> NUMBER OF SEQ ID NOS: 35
 45 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

49 <210> SEQ ID NO: 1
 51 <211> LENGTH: 600
 53 <212> TYPE: DNA
 55 <213> ORGANISM: Mus musculus
 59 <220> FEATURE:
 61 <221> NAME/KEY: CDS
 63 <222> LOCATION: (1)..(600)
 67 <400> SEQUENCE: 1
 E--> 68 atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc ttc cta atc aga
 69 48
 70 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
 71 1 5 10 15
 E--> 73 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca
 74 96
 75 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 76 20 25 30
 E--> 78 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc
 79 144
 80 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 81 35 40 45
 E--> 83 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa
 84 192
 85 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 86 50 55 60
 E--> 88 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca
 89 240

48
 format
 even

96

↓

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90 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
91 65              70              75              80
E--> 93 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta
94 288
95 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
96              85              90              95
E--> 98 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc
99 336
100 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
101              100              105              110
E--> 103 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat
104 384
105 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
106              115              120              125
E--> 108 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta
109 432
110 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
111              130              135              140
E--> 113 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata
114 480
115 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
116 145              150              155              160
E--> 118 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac
119 528
120 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
121              165              170              175
E--> 123 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag
124 576
125 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
126              180              185              190
E--> 128 tct aga ctt gca ggt gtg acc tca
129 600
130 Ser Arg Leu Ala Gly Val Thr Ser
131              195              200
378 <210> SEQ ID NO: 6
380 <211> LENGTH: 966
382 <212> TYPE: DNA
384 <213> ORGANISM: Mus musculus
388 <220> FEATURE:
390 <221> NAME/KEY: CDS
392 <222> LOCATION: (1)..(966)
396 <400> SEQUENCE: 6
E--> 397 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct
398 48
399 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
400 1              5              10              15
E--> 402 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt
403 96
404 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly

```

*same
env*

same

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      405              20              25              30
E--> 407 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act
      408 144
      409 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
      410              35              40              45
E--> 412 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac
      413 192
      414 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
      415              50              55              60
E--> 417 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa
      418 240
      419 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
      420 65              70              75              80
E--> 422 atc gaa aac cca gaa gtt tgc gtg act tac tac ctg cct tac aag tct
      423 288
      424 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
      425              85              90              95
E--> 427 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc
      428 336
      429 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
      430              100              105              110
E--> 432 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc
      433 384
      434 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
      435              115              120              125
E--> 437 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca
      438 432
      439 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
      440              130              135              140
E--> 442 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg
      443 480
      444 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
      445 145              150              155              160
E--> 447 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac
      448 528
      449 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
      450              165              170              175
E--> 452 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca
      453 576
      454 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
      455              180              185              190
E--> 457 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac
      458 624
      459 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
      460              195              200              205
E--> 462 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat
      463 672
      464 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
      465              210              215              220

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E--> 467 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt
      468 720
      469 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
      470 225                230                235                240
E--> 472 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att
      473 768
      474 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
      475                245                250                255
E--> 477 agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa
      478 816
      479 Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
      480                260                265                270
E--> 482 acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg
      483 864
      484 Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
      485                275                280                285
E--> 487 gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc
      488 912
      489 Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
      490                290                295                300
E--> 492 cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac
      493 960
      494 His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
      495 305                310                315                320
E--> 497 cac gcc
      498 966
      499 His Ala
      831 <210> SEQ ID NO: 11
      833 <211> LENGTH: 864
      835 <212> TYPE: DNA
      837 <213> ORGANISM: Homo sapiens
      841 <220> FEATURE:
      843 <221> NAME/KEY: CDS
      845 <222> LOCATION: (1)..(864)
      849 <400> SEQUENCE: 11
E--> 850 atg cgg ctg ggc agt cct gga ctg ctc ttc ctg ctc ttc agc agc ctt
      851 48
      852 Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
      853 1                5                10                15
E--> 855 cga gct gat act cag gag aag gaa gtc aga gcg atg gta ggc agc gac
      856 96
      857 Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
      858                20                25                30
E--> 860 gtg gag ctc agc tgc gct tgc cct gaa gga agc cgt ttt gat tta aat
      861 144
      862 Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
      863                35                40                45
E--> 865 gat gtt tac gta tat tgg caa acc agt gag tcg aaa acc gtg gtg acc
      866 192

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*same**same*

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      867 Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
      868      50                      55                      60
E--> 870 tac cac atc cca cag aac agc tcc ttg gaa aac gtg gac agc cgc tac
      871 240
      872 Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
      873 65                      70                      75                      80
E--> 875 cgg aac cga gcc ctg atg tca ccg gcc ggc atg ctg cgg ggc gac ttc
      876 288
      877 Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
      878                      85                      90                      95
E--> 880 tcc ctg cgc ttg ttc aac gtc acc ccc cag gac gag cag aag ttt cac
      881 336
      882 Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
      883                      100                      105                      110
E--> 885 tgc ctg gtg ttg agc caa tcc ctg gga ttc cag gag gtt ttg agc gtt
      886 384
      887 Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
      888                      115                      120                      125
E--> 890 gag gtt aca ctg cat gtg gca gca aac ttc agc gtg ccc gtc gtc agc
      891 432
      892 Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
      893                      130                      135                      140
E--> 895 gcc ccc cac agc ccc tcc cag gat gag ctc acc ttc acg tgt aca tcc
      896 480
      897 Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
      898                      145                      150                      155                      160
E--> 900 ata aac ggc tac ccc agg ccc aac gtg tac tgg atc aat aag acg gac
      901 528
      902 Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
      903                      165                      170                      175
E--> 905 aac agc ctg ctg gac cag gct ctg cag aat gac acc gtc ttc ttg aac
      906 576
      907 Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
      908                      180                      185                      190
E--> 910 atg cgg ggc ttg tat gac gtg gtc agc gtg ctg agg atc gca cgg acc
      911 624
      912 Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
      913                      195                      200                      205
E--> 915 ccc agc gtg aac att ggc tgc tgc ata gag aac gtg ctt ctg cag cag
      916 672
      917 Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
      918                      210                      215                      220
E--> 920 aac ctg act gtc ggc agc cag aca gga aat gac atc gga gag aga gac
      921 720
      922 Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
      923 225                      230                      235                      240
E--> 925 aag atc aca gag aat cca gtc agt acc ggc gag aaa aac gcg gcc acg
      926 768
      927 Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr

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Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

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928          245          250          255
E--> 930 tgg agc atc ctg gct gtc ctg tgc ctg ctt gtg gtc gtg gcg gtg gcc
931 816
932 Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
933          260          265          270
E--> 935 ata ggc tgg gtg tgc agg gac cga tgc ctc caa cac agc tat gca ggt
936 864
937 Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
938          275          280          285
1230 <210> SEQ ID NO: 16
1232 <211> LENGTH: 1294
1234 <212> TYPE: DNA
1236 <213> ORGANISM: Homo sapiens
1240 <220> FEATURE:
1242 <221> NAME/KEY: 5'UTR
1244 <222> LOCATION: (1)..(199)
1248 <220> FEATURE:
1250 <221> NAME/KEY: CDS
1252 <222> LOCATION: (200)..(1105)
1256 <400> SEQUENCE: 16
E--> 1257 gctggtacgc ctgcaggtag cggtccggaa ttcccggtgc gaccacgcgc tccgccacgc
1258 60
E--> 1260 cgtccgcggg agcgcagtta gacccgatct cccgcgcccc gaggttgctc ctctccgagg
1261 120
E--> 1263 tctccgcggg cccaagttct ccgcgccccg aggtctccgc gccccgaggt ctccgcggcc
1264 180
E--> 1266 cgaggtctcc gcccgacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg
1267 232
1268          Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu
1269          1          5          10
E--> 1271 ctc ttc agc agc ctt cga gct gat act cag gag aag gaa gtc aga gcg
1272 280
1273 Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala
1274          15          20          25
E--> 1276 atg gta ggc agc gac gtg gag ctc agc tgc gct tgc cct gaa gga agc
1277 328
1278 Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser
1279          30          35          40
E--> 1281 cgt ttt gat tta aat gat gtt tac gta tat tgg caa acc agt gag tcg
1282 376
1283 Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser
1284          45          50          55
E--> 1286 aaa acc gtg gtg acc tac cac atc cca cag aac agc tcc ttg gaa aac
1287 424
1288 Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn
1289 60          65          70          75
E--> 1291 gtg gac agc cgc tac cgg aac cga gcc ctg atg tca ccg gcc ggc atg
1292 472
1293 Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met

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1294      80      85      90
E--> 1296 ctg cgg ggc gac ttc tcc ctg cgc ttg ttc aac gtc acc ccc cag gac
1297 520
1298 Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp
1299      95      100      105
E--> 1301 gag cag aag ttt cac tgc ctg gtg ttg agc caa tcc ctg gga ttc cag
1302 568
1303 Glu Gln Lys Phe His Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln
1304      110      115      120
E--> 1306 gag gtt ttg agc gtt gag gtt aca ctg cat gtg gca gca aac ttc agc
1307 616
1308 Glu Val Leu Ser Val Glu Val Thr Leu His Val Ala Ala Asn Phe Ser
1309      125      130      135
E--> 1311 gtg ccc gtc gtc agc gcc ccc cac agc ccc tcc cag gat gag ctc acc
1312 664
1313 Val Pro Val Val Ser Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr
1314      140      145      150      155
E--> 1316 ttc acg tgt aca tcc ata aac ggc tac ccc agg ccc aac gtg tac tgg
1317 712
1318 Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp
1319      160      165      170
E--> 1321 atc aat aag acg gac aac agc ctg ctg gac cag gct ctg cag aat gac
1322 760
1323 Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp
1324      175      180      185
E--> 1326 acc gtc ttc ttg aac atg cgg ggc ttg tat gac gtg gtc agc gtg ctg
1327 808
1328 Thr Val Phe Leu Asn Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu
1329      190      195      200
E--> 1331 agg atc gca cgg acc ccc agc gtg aac att ggc tgc tgc ata gag aac
1332 856
1333 Arg Ile Ala Arg Thr Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn
1334      205      210      215
E--> 1336 gtg ctt ctg cag cag aac ctg act gtc ggc agc cag aca gga aat gac
1337 904
1338 Val Leu Leu Gln Gln Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp
1339      220      225      230      235
E--> 1341 atc gga gag aga gac aag atc aca gag aat cca gtc agt acc ggc gag
1342 952
1343 Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu
1344      240      245      250
E--> 1346 aaa aac gcg gcc acg tgg agc atc ctg gct gtc ctg tgc ctg ctt gtg
1347 1000
1348 Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val
1349      255      260      265
E--> 1351 gtc gtg gcg gtg gcc ata ggc tgg gtg tgc agg gac cga tgc ctc caa
1352 1048
1353 Val Val Ala Val Ala Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln
1354      270      275      280

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E--> 1356 cac agc tat gca ggt gcc tgg gct gtg agt ccg gag aca gag ctc act
      1357 1096
      1358 His Ser Tyr Ala Gly Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr
      1359      285              290              295
E--> 1361 ggc cac gtt tgaccggagc tcaccgcca gagcgtggac agggcttccg
      1362 1145
      1363 Gly His Val
      1364 300
E--> 1366 tgagacgcca ccgtgagagg ccaggtggca gcttgagcat ggactccag actgcagggg
      1367 1205
E--> 1369 agcacttggg gcagcccca gaaggaccac tgctggatcc cagggagaac ctgctggcgt
      1370 1265
E--> 1372 tggctgtgat cctggaatga ggccctttc
      1373 1294
      1693 <210> SEQ ID NO: 21
      1695 <211> LENGTH: 1370
      1697 <212> TYPE: DNA
      1699 <213> ORGANISM: Homo sapiens
      1703 <220> FEATURE:
      1705 <221> NAME/KEY: 5'UTR
      1707 <222> LOCATION: (1)..(165)
      1711 <220> FEATURE:
      1713 <221> NAME/KEY: CDS
      1715 <222> LOCATION: (166)..(762)
      1719 <400> SEQUENCE: 21
E--> 1720 aacaatttca cacaggaaac agctatgacc atgattacgc caagctctaa tacgactcac
      1721 60
E--> 1723 tatagggaaa gctggtacgc ctgcaggtac cgggccggaa ttcccgggtc gaccacgcg
      1724 120
E--> 1726 tccgtgaaca ctgaacgca ggactgttaa ctgtttctgg caaac atg aag tca ggc
      1727 177
      1728
      1729 Met Lys Ser Gly
      1
E--> 1731 ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga
      1732 225
      1733 Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
      1734 5              10              15              20
E--> 1736 gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga
      1737 273
      1738 Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
      1739      25              30              35
E--> 1741 ggt gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa
      1742 321
      1743 Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
      1744      40              45              50
E--> 1746 atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca
      1747 369
      1748 Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
      1749      55              60              65

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DATE: 08/20/2002

PATENT APPLICATION: US/09/728,421D

TIME: 12:49:42

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

```

E--> 1751 aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat
      1752 417
      1753 Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
      1754      70                      75                      80
E--> 1756 tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac
      1757 465
      1758 Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
      1759 85                      90                      95                      100
E--> 1761 cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct
      1762 513
      1763 His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
      1764      105                      110                      115
E--> 1766 cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa
      1767 561
      1768 Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
      1769      120                      125                      130
E--> 1771 tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca
      1772 609
      1773 Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
      1774      135                      140                      145
E--> 1776 gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt
      1777 657
      1778 Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
      1779      150                      155                      160
E--> 1781 aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac
      1782 705
      1783 Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
      1784 165                      170                      175                      180
E--> 1786 atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat
      1787 753
      1788 Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
      1789      185                      190                      195
E--> 1791 gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc
      1792 802
      1793 Val Thr Leu
E--> 1796 cagttttcct caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac
      1797 862
E--> 1799 ttaactacat acatcttctg ctggtgtttt gttcaatctg gaagaatgac tgtatcagtc
      1800 922
E--> 1802 aatgggggatt ttaacagact gccttgggtac tgccgagtcc tctcaaaaca aacaccctct
      1803 982
E--> 1805 tgcaaccagc tttggagaaa gccagctcc tgtgtgctca ctgggagtgg aatccctgtc
      1806 1042
E--> 1808 tccacatctg ctctagcag tgcatcagcc agtaaaacaa acacatttac aagaaaaatg
      1809 1102
E--> 1811 ttttaaagat gccaggggta ctgaatctgc aaagcaaatg agcagccaag gaccagcatc
      1812 1162
E--> 1814 tgtccgcatt tcactatcat actacctctt ctttctgtag ggatgagaat tcctctttta
      1815 1222

```



RAW SEQUENCE LISTING

DATE: 08/20/2002

PATENT APPLICATION: US/09/728,421D

TIME: 12:49:42

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

E--> 1817 atcagtcaag ggagatgctt caaagctgga gctattttat ttctgagatg ttgatgtgaa
1818 1282

E--> 1820 ctgtacatta gtacatactc agtactctcc ttcaattgct gaaccccagt tgaccatttt
1821 1342

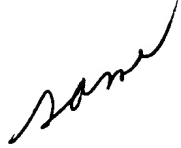
E--> 1823 accaagactt tagatgcttt cttgtgcc
1824 1370
1993 <210> SEQ ID NO: 25
1995 <211> LENGTH: 24
1997 <212> TYPE: DNA
1999 <213> ORGANISM: Artificial Sequence
2003 <220> FEATURE:
2005 <221> NAME/KEY: misc_feature
2007 <223> OTHER INFORMATION: Synthetic oligonucleotide
2011 <400> SEQUENCE: 25

E--> 2012 accatgcggc tgggcagtcc tgga
2013 24
2016 <210> SEQ ID NO: 26
2018 <211> LENGTH: 23
2020 <212> TYPE: DNA
2022 <213> ORGANISM: Artificial Sequence
2026 <220> FEATURE:
2028 <221> NAME/KEY: misc_feature
2030 <223> OTHER INFORMATION: Synthetic oligonucleotide
2034 <400> SEQUENCE: 26

E--> 2035 tggtagaccta ccacatccca cag
2036 23
2039 <210> SEQ ID NO: 27
2041 <211> LENGTH: 23
2043 <212> TYPE: DNA
2045 <213> ORGANISM: Artificial Sequence
2049 <220> FEATURE:
2051 <221> NAME/KEY: misc_feature
2053 <223> OTHER INFORMATION: Synthetic oligonucleotide
2057 <400> SEQUENCE: 27

E--> 2058 tccgatgtca tttcctgtct ggc
2059 23
2062 <210> SEQ ID NO: 28
2064 <211> LENGTH: 24
2066 <212> TYPE: DNA
2068 <213> ORGANISM: Artificial Sequence
2072 <220> FEATURE:
2074 <221> NAME/KEY: misc_feature
2076 <223> OTHER INFORMATION: Synthetic oligonucleotide
2080 <400> SEQUENCE: 28

E--> 2081 gctctgtctc cggactcaca gccc
2082 24
2085 <210> SEQ ID NO: 29
2087 <211> LENGTH: 28
2089 <212> TYPE: DNA




RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/728,421D

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TIME: 12:49:42

Input Set : A:\pto_vsk.txt
Output Set: N:\CRF4\08202002\I728421D.raw

2091 <213> ORGANISM: Artificial Sequence
2095 <220> FEATURE:
2097 <221> NAME/KEY: misc_feature
2099 <223> OTHER INFORMATION: Synthetic oligonucleotide
2103 <400> SEQUENCE: 29
E--> 2104 gtggcagcaa acttcagcgt gcccgtcg
2105 28
2108 <210> SEQ ID NO: 30
2110 <211> LENGTH: 28
2112 <212> TYPE: DNA
2114 <213> ORGANISM: Artificial Sequence
2118 <220> FEATURE:
2120 <221> NAME/KEY: misc_feature
2122 <223> OTHER INFORMATION: Synthetic oligonucleotide
2126 <400> SEQUENCE: 30
E--> 2127 cccaacgtgt actggatcaa taagacgg
2128 28
2131 <210> SEQ ID NO: 31
2133 <211> LENGTH: 28
2135 <212> TYPE: DNA
2137 <213> ORGANISM: Artificial Sequence
2141 <220> FEATURE:
2143 <221> NAME/KEY: misc_feature
2145 <223> OTHER INFORMATION: Synthetic oligonucleotide
2149 <400> SEQUENCE: 31
E--> 2150 gcgtgctgag gatcgacgg acccccag
2151 28
2154 <210> SEQ ID NO: 32
2156 <211> LENGTH: 21
2158 <212> TYPE: DNA
2160 <213> ORGANISM: Artificial Sequence
2164 <220> FEATURE:
2166 <221> NAME/KEY: misc_feature
2168 <223> OTHER INFORMATION: Synthetic oligonucleotide
2172 <400> SEQUENCE: 32
E--> 2173 gcctctagaa agagctggga c
2174 21
2177 <210> SEQ ID NO: 33
2179 <211> LENGTH: 21
2181 <212> TYPE: DNA
2183 <213> ORGANISM: Artificial Sequence
2187 <220> FEATURE:
2189 <221> NAME/KEY: misc_feature
2191 <223> OTHER INFORMATION: Synthetic oligonucleotide
2195 <400> SEQUENCE: 33
E--> 2196 cgccgtgttc catttatgag c
2197 21
2200 <210> SEQ ID NO: 34
2202 <211> LENGTH: 18



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DATE: 08/20/2002


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Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

2204 <212> TYPE: DNA
2206 <213> ORGANISM: Artificial Sequence
2210 <220> FEATURE:
2212 <221> NAME/KEY: misc_feature
2214 <223> OTHER INFORMATION: Synthetic oligonucleotide
2218 <400> SEQUENCE: 34
E--> 2219 gcatatttat gaatccca
2220 18
2223 <210> SEQ ID NO: 35
2225 <211> LENGTH: 18
2227 <212> TYPE: DNA
2229 <213> ORGANISM: Artificial Sequence
2233 <220> FEATURE:
2235 <221> NAME/KEY: misc_feature
2237 <223> OTHER INFORMATION: Synthetic oligonucleotide
2241 <400> SEQUENCE: 35
E--> 2242 actattaggg tcatgcac
2243 18



VERIFICATION SUMMARY

DATE: 08/20/2002

PATENT APPLICATION: US/09/728,421D

TIME: 12:49:43

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

L:68 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:1

M:254 Repeated in SeqNo=1

L:333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16

L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:32

L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:48

L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:64

L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:80

L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:96

L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:112

L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:128

L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:144

L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:160

L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:176

L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:192

L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:208

L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:224

L:397 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:6

M:254 Repeated in SeqNo=6

L:768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0

L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16

L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32

L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48

L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:64

L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:80

L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:96

L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:112

L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:128

L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:144

L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:160

L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:176

L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192

L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:208

L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:224

L:813 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:240

L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:256

L:819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:272

L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:288

L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:304

L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:320

L:850 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:11

M:254 Repeated in SeqNo=11

L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

L:1179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:16

L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:32

L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48

L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:64

L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:80

VERIFICATION SUMMARY

DATE: 08/20/2002

PATENT APPLICATION: US/09/728,421D

TIME: 12:49:43

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF4\08202002\I728421D.raw

L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:96
L:1197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:112
L:1200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:128
L:1203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:144
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:160
L:1209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:176
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:192
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:208
L:1257 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:16
M:254 Repeated in SeqNo=16
L:1720 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
M:254 Repeated in SeqNo=21
L:2012 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:25
L:2035 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:26
L:2058 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:27
L:2081 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:28
L:2104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:29
L:2127 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:30
L:2150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:31
L:2173 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:32
L:2196 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:33
L:2219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:34
L:2242 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:35



RAW SEQUENCE LISTING

DATE: 08/21/2002

PATENT APPLICATION: US/09/728,421D

TIME: 20:14:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08212002\I728421D.raw

5 <110> APPLICANT: Yoshinaga, Steven
 9 <120> TITLE OF INVENTION: Novel Polypeptides Involved in Immune Response
 13 <130> FILE REFERENCE: A-579D
 17 <140> CURRENT APPLICATION NUMBER: 09/728,421D
 19 <141> CURRENT FILING DATE: 2000-11-28
 23 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
 25 <151> PRIOR FILING DATE: 2000-01-27
 29 <150> PRIOR APPLICATION NUMBER: US 09/264,527
 31 <151> PRIOR FILING DATE: 1999-03-08
 35 <150> PRIOR APPLICATION NUMBER: US 09/244,448
 37 <151> PRIOR FILING DATE: 1999-02-03
 41 <160> NUMBER OF SEQ ID NOS: 35
 45 <170> SOFTWARE: PatentIn version 3.0
 49 <210> SEQ ID NO: 1
 51 <211> LENGTH: 600
 53 <212> TYPE: DNA
 55 <213> ORGANISM: Mus musculus
 59 <220> FEATURE:
 61 <221> NAME/KEY: CDS
 63 <222> LOCATION: (1)..(600)
 67 <400> SEQUENCE: 1

68	atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc ttc cta atc aga	48
69	Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg	
70	1 5 10 15	
72	ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca	96
73	Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser	
74	20 25 30	
76	ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc	144
77	Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val	
78	35 40 45	
80	cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa	192
81	Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu	
82	50 55 60	
84	ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca	240
85	Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro	
86	65 70 75 80	
88	atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta	288
89	Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
90	85 90 95	
92	aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc	336
93	Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser	
94	100 105 110	
96	att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat	384

mg-7

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DATE: 08/21/2002

TIME: 20:14:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08212002\I728421D.raw

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97 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
98      115      120      125
100 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432
101 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
102      130      135      140
104 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480
105 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
106 145      150      155      160
108 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528
109 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
110      165      170      175
112 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576
113 Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys
114      180      185      190
116 tct aga ctt gca ggt gtg acc tca 600
117 Ser Arg Leu Ala Gly Val Thr Ser
118      195      200
121 <210> SEQ ID NO: 2
123 <211> LENGTH: 200
125 <212> TYPE: PRT
127 <213> ORGANISM: Mus musculus
131 <400> SEQUENCE: 2
133 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
134 1      5      10      15
137 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
138      20      25      30
141 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
142      35      40      45
145 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
146      50      55      60
149 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
150 65      70      75      80
153 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
154      85      90      95
157 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
158      100      105      110
161 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
162      115      120      125
165 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
166      130      135      140
169 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
170 145      150      155      160
173 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
174      165      170      175
177 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
178      180      185      190
181 Ser Arg Leu Ala Gly Val Thr Ser
182      195      200
185 <210> SEQ ID NO: 3

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DATE: 08/21/2002

PATENT APPLICATION: US/09/728,421D

TIME: 20:14:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08212002\I728421D.raw

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187 <211> LENGTH: 200
189 <212> TYPE: PRT
191 <213> ORGANISM: Mus musculus
195 <400> SEQUENCE: 3
197 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
198 1 5 10 15
200 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
201 20 25 30
203 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
204 35 40 45
206 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
207 50 55 60
209 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
210 65 70 75 80
212 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
213 85 90 95
215 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
216 100 105 110
218 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
219 115 120 125
221 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
222 130 135 140
224 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
225 145 150 155 160
227 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
228 165 170 175
230 Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys
231 180 185 190
233 Ser Arg Leu Ala Gly Val Thr Ser
234 195 200
236 <210> SEQ ID NO: 4
238 <211> LENGTH: 218
240 <212> TYPE: PRT
242 <213> ORGANISM: Mus musculus
246 <400> SEQUENCE: 4
248 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
249 1 5 10 15
251 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
252 20 25 30
254 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
255 35 40 45
257 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
258 50 55 60
260 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
261 65 70 75 80
263 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
264 85 90 95
266 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
267 100 105 110

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RAW SEQUENCE LISTING

DATE: 08/21/2002

PATENT APPLICATION: US/09/728,421D

TIME: 20:14:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08212002\I728421D.raw

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269 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
270      115      120      125
272 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
273      130      135      140
275 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
276 145      150      155      160
278 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
279      165      170      175
281 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
282      180      185      190
284 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
285      195      200      205
287 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
288      210      215
290 <210> SEQ ID NO: 5
292 <211> LENGTH: 234
294 <212> TYPE: PRT
296 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
302 <221> NAME/KEY: misc_feature
304 <222> LOCATION: (1)..(234)
306 <223> OTHER INFORMATION: Xaa is an unspecified amino acid
310 <220> FEATURE:
312 <221> NAME/KEY: misc_feature
314 <223> OTHER INFORMATION: Synthetic
318 <400> SEQUENCE: 5
W--> 320 Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
321 1      5      10      15
W--> 323 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
324      20      25      30
W--> 326 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
327      35      40      45
W--> 329 Val Xaa Xaa Ser Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
330      50      55      60
W--> 332 Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Cys Xaa
333 65      70      75      80
W--> 335 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
336      85      90      95
W--> 338 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Val Xaa Phe Xaa Leu
339      100      105      110
W--> 341 Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Cys Xaa Xaa Xaa
342      115      120      125
W--> 344 Xaa Xaa Xaa Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Gly Xaa
345      130      135      140
W--> 347 Xaa Xaa His Ile Xaa Glu Xaa Xaa Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa
348 145      150      155      160
W--> 350 Lys Leu Xaa Trp Xaa Leu Xaa Val Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa
351      165      170      175
W--> 353 Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Ile Trp Xaa Xaa Xaa

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,421D

DATE: 08/21/2002
 TIME: 20:14:28

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF4\08212002\I728421D.raw

```

354          180          185          190
W--> 356 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa
357          195          200          205
W--> 359 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
360          210          215          220
W--> 362 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
363 225          230
365 <210> SEQ ID NO: 6
367 <211> LENGTH: 966
369 <212> TYPE: DNA
371 <213> ORGANISM: Mus musculus
375 <220> FEATURE:
377 <221> NAME/KEY: CDS
379 <222> LOCATION: (1)..(966)
383 <400> SEQUENCE: 6
384 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct      48
385 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
386 1          5          10          15
388 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
389 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
390          20          25          30
392 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act      144
393 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
394          35          40          45
396 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac      192
397 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
398          50          55          60
400 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa      240
401 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
402 65          70          75          80
404 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct      288
405 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
406          85          90          95
408 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc      336
409 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
410          100          105          110
412 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc      384
413 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
414          115          120          125
416 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca      432
417 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
418          130          135          140
420 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg      480
421 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
422 145          150          155          160
424 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac      528
425 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
426          165          170          175
428 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca      576

```

RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/09/728,421D

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Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF4\08212002\I728421D.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,19,20,21,22,23,24,25,26
 Seq#:5; Xaa Pos. 27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
 Seq#:5; Xaa Pos. 46,47,48,50,51,54,56,57,58,59,60,61,62,63,64,65,66,67,69
 Seq#:5; Xaa Pos. 70,71,72,73,74,75,77,78,80,81,82,83,84,85,86,87,88,89,90
 Seq#:5; Xaa Pos. 91,92,93,94,95,96,97,98,100,101,102,103,104,106,107,109
 Seq#:5; Xaa Pos. 111,113,115,116,117,118,119,120,121,122,126,127,128,129
 Seq#:5; Xaa Pos. 130,131,135,136,137,138,139,140,142,144,145,146,149,151
 Seq#:5; Xaa Pos. 152,155,156,157,158,159,160,163,165,167,169,170,171,172
 Seq#:5; Xaa Pos. 173,175,176,177,178,181,182,183,184,186,187,190,191,192
 Seq#:5; Xaa Pos. 193,194,195,196,197,198,199,200,201,202,203,204,205,206
 Seq#:5; Xaa Pos. 208,209,210,211,212,213,214,215,216,217,218,219,220,221
 Seq#:5; Xaa Pos. 222,223,225,226,228,229,230,231,232,233,234
 Seq#:10; Xaa Pos. 2,3,4,6,8,9,10,12,13,14,15,17,18,19,20,22,23,24,25,26,27
 Seq#:10; Xaa Pos. 28,29,30,32,35,38,39,40,42,43,44,45,46,47,48,49,50,51,52
 Seq#:10; Xaa Pos. 53,54,56,57,58,60,62,64,65,66,67,68,69,71,72,73,75,76,77
 Seq#:10; Xaa Pos. 78,82,83,84,85,86,88,89,90,91,92,94,95,96,97,98,99,100
 Seq#:10; Xaa Pos. 101,103,104,105,110,111,112,113,115,116,117,118,119,120
 Seq#:10; Xaa Pos. 121,122,125,126,127,128,129,130,131,132,134,135,136,137
 Seq#:10; Xaa Pos. 138,140,142,143,144,145,146,147,148,149,150,151,152,153
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 Seq#:10; Xaa Pos. 177,178,179,180,181,183,184,187,188,189,190,192,194,196
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 Seq#:10; Xaa Pos. 215,216,217,218,219,220,221,222,223,224,225,226,227,228
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 Seq#:10; Xaa Pos. 259,260,261,262,263,264,265,266,268,269,270,271,272,273
 Seq#:10; Xaa Pos. 274,275,276,277,278,279,280,281,283,285,287,288,289,290
 Seq#:10; Xaa Pos. 291,292,293,294,295,296,297,298,300,301,302,303,304,305
 Seq#:10; Xaa Pos. 307,308,309,310,312,314,317,318,319,320,321,323,325,326
 Seq#:10; Xaa Pos. 327
 Seq#:15; Xaa Pos. 2,5,11,13,17,18,20,21,22,23,25,27,28,29,35,36,37,38,39,40
 Seq#:15; Xaa Pos. 41,45,46,48,49,51,52,53,58,60,63,64,65,67,68,69,71,72,74
 Seq#:15; Xaa Pos. 78,80,87,89,91,93,95,96,97,98,99,100,101,102,103,104,105
 Seq#:15; Xaa Pos. 107,108,109,111,113,120,123,125,126,127,129,130,131,132
 Seq#:15; Xaa Pos. 133,135,137,140,142,147,150,155,161,163,168,171,174,175
 Seq#:15; Xaa Pos. 181,183,186,187,188,190,191,192,193,194,195,198,202,204
 Seq#:15; Xaa Pos. 207,209,210,213,214,215,216,217,219,220,222,223,224,225
 Seq#:15; Xaa Pos. 226,227,228,229,230,231,233,234,235,236,237,238,239,244
 Seq#:15; Xaa Pos. 245,246,247,248,250,251,252,254,255,256,257,259,261,262
 Seq#:15; Xaa Pos. 263,264,267,269,270,271,272,273,274,275,276,277,278,279
 Seq#:15; Xaa Pos. 280
 Seq#:20; Xaa Pos. 2,4,5,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
 Seq#:20; Xaa Pos. 25,26,27,28,29,32,35,38,42,44,45,46,48,51,57,59,63,64,66
 Seq#:20; Xaa Pos. 67,68,69,71,73,74,75,81,82,83,84,85,86,87,91,92,94,95,97

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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\08212002\I728421D.raw

Seq#:20; Xaa Pos. 98,99,104,106,109,110,111,113,114,115,117,118,120,124,126
Seq#:20; Xaa Pos. 133,135,137,139,141,142,143,144,145,146,147,148,149,150
Seq#:20; Xaa Pos. 151,153,154,155,157,159,166,169,171,172,173,175,176,177
Seq#:20; Xaa Pos. 178,179,181,183,186,188,193,196,201,207,209,214,217,220
Seq#:20; Xaa Pos. 221,227,229,232,233,234,236,237,238,239,240,241,244,248
Seq#:20; Xaa Pos. 250,253,255,256,259,260,261,262,263,265,266,267,269,270
Seq#:20; Xaa Pos. 271,272,273,274,275,276,277,278,280,281,282,283,284,285
Seq#:20; Xaa Pos. 286,291,292,293,294,295,297,298,299,301,302,303,304,306
Seq#:20; Xaa Pos. 308,309,310,311,314,316,317,318,320,321,323,324,327,329